RAW SEQUENCE LISTING DATE: 03/27/2001
PATENT APPLICATION: US/09/316,048A TIME: 07:17:16

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Output Set: N:\CRF3\03272001\I316048A.raw

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 3 <110> APPLICANT: MOULAND, Andrew J.
 4       COHEN, Eric A.
 5       WICKHAM, Louise
 6       LUO, Ming
 7       DUCHAINE, Thomas
 9 <120> TITLE OF INVENTION: MAMMALIAN STAUFEN AND USE THEREOF
11 <130> FILE REFERENCE: 10875-77
13 <140> CURRENT APPLICATION NUMBER: 09/316,048A
14 <141> CURRENT FILING DATE: 1999-05-21
16 <150> PRIOR APPLICATION NUMBER: CA 2,238,656
17 <151> PRIOR FILING DATE: 1998-05-22
19 <160> NUMBER OF SEQ ID NOS: 27
21 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
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30 <222> LOCATION: (3)..(1775)
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37 ggc ggc tgc gcg tct ctc tcg gct ccc gct tcc ttt gac cgc ctc ccc   95
38 Gly Gly Cys Ala Ser Leu Ser Ala Pro Ala Ser Phe Asp Arg Leu Pro
39                  20                  25                  30
41 ccc ccg gcc cgg cgg cgc ccg cct cct cca cgg cca ctc cgc ctc ttc   143
42 Pro Pro Ala Arg Arg Arg Pro Pro Pro Pro Arg Pro Leu Arg Leu Phe
43              35                  40                  45
45 cct ccc ttc gtc cct tct tcc tct ccc ttt ttt cct tct tcc ttc ccc   191
46 Pro Pro Phe Val Pro Ser Ser Ser Pro Phe Phe Pro Ser Ser Phe Pro
47          50                  55                  60
49 tcc tcg ccg cca ccg ccc agg acc gcc ggc cgg ggg acg agc tcg gag   239
50 Ser Ser Pro Pro Pro Pro Arg Thr Ala Gly Arg Gly Thr Ser Ser Glu
51      65                  70                  75
53 cag cag cca gaa agc ata acc cct act gta gaa cta aat gca ctg tgc   287
54 Gln Gln Pro Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys
55  80                  85                  90                  95
57 atg aaa ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac tct   335
58 Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser
59                 100                 105                 110
61 cgg atg cag tcc acc tat aac tac aac atg aga gga ggt gct tat ccc   383
62 Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro
63             115                 120                 125
65 ccg agg tac ttt tac cca ttt cca gtt cca cct tta ctt tat caa gtg   431
66 Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val
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70 Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg
71      145                 150                 155
73 cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg cag   527
74 Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln
75 160                 165                 170                 175
77 aat gag ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc gaa   575
78 Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu
79                  180                 185                 190
81 gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att gca   623
82 Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala
83              195                 200                 205
85 ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt ggc   671
86 Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly
87          210                 215                 220
89 cca ccc cac atg aag aac ttt gtg acc aag gtt tcg gtt ggg gag ttt   719
90 Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe
91      225                 230                 235
93 gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc   767
94 Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala
95 240                 245                 250                 255
97 gcc ata gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca   815
98 Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala
99                  260                 265                 270
101 gtt gaa cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc   863
102 Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val
103             275                 280                 285
105 aag cca cag aca agc cca gaa tat ggc cag ggg atc aat ccg att agc   911
106 Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser
107         290                 295                 300
109 cga ctg gcc cag atc cag cag gca aaa aag gag aag gag cca gag tac   959
110 Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr
111     305                 310                 315
113 acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg atg   1007
114 Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met
115 320                 325                 330                 335
117 cag gtg aag gtt gga aac cac act gca gaa gga acg ggc acc aac aag   1055
118 Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys
119                 340                 345                 350
121 aag gtg gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt ggt   1103
122 Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly
123             355                 360                 365
125 ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca gag   1151
126 Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu
127         370                 375                 380
129 gag aag aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc ttt   1199
130 Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe
131     385                 390                 395
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137 gag ttc agg atg cct tat cta agt cat cag cag ctg cct gct gga att   1295
138 Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile
139                 420                 425                 430
141 ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa gga   1343
142 Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly
143             435                 440                 445
145 cat cac acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag gcc   1391
146 His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala
147         450                 455                 460
149 acg gta act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc tcg   1439
150 Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser
151     465                 470                 475
153 ccc aca gcc gag acc att tta aag aat aac atc tct tca ggc cac gta   1487
154 Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val
155 480                 485                 490                 495
157 ccc cat gga cct ctc acg aga ccc tct gag caa ctg gac tat ctt tcc   1535
158 Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser
159                 500                 505                 510
161 aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac aac   1583
162 Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn
163             515                 520                 525
165 aag aac gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct ctg   1631
166 Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu
167         530                 535                 540
169 atc agc cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg gct   1679
170 Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala
171     545                 550                 555
173 gcg ctg aac atc tta aag ttg ctg tct gag ttg gac caa caa agt aca   1727
174 Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr
175 560                 565                 570                 575
177 gag atg cca aga aca gga aac gga cca atg tct gtg tgt ggg agg tgc   1775
178 Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys
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185 aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg tggccggctg 1955
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193 cacgacccct tctcaagctg gctcactcag acacattggg acaaaccctg gacagccatg 2195
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197 ctactcagcg tgacccaact tttctagtgt gccacggccc caccacctcc tgcagtaccc 2315
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201 ttttgattga tatgacacta tataaaattt tcatttgaga atttctcaat tgtatctagt 2435
203 taaatagcac agtttggaaa cttgtctgag actgacttta tcaataatct aaccgacaaa 2495
205 gatcatatcc atgtgtatgt ggttagacat ttttatttca ttgactaacc caggacagtt 2555
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211 gatcatttgg ttccattttt atttcatttt tatttttgtt aatgcaaaca ggacttaaat 2735
213 gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata catatggctc 2795
215 ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc atataaacct 2855
217 gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag ggctgaaaag 2915
219 aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac tgtacacaga 2975
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238              20                  25                  30
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241          35                  40                  45
243 Pro Phe Val Pro Ser Ser Ser Pro Phe Phe Pro Ser Ser Phe Pro Ser
244      50                  55                  60
246 Ser Pro Pro Pro Pro Arg Thr Ala Gly Arg Gly Thr Ser Ser Glu Gln
247  65                  70                  75                  80
249 Gln Pro Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met
250                  85                  90                  95
252 Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg
253             100                 105                 110
255 Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro
256         115                 120                 125
258 Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu
259     130                 135                 140
261 Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln
262 145                 150                 155                 160
264 Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn
265                 165                 170                 175
267 Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu
268             180                 185                 190
270 Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu
271         195                 200                 205
273 Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro
274     210                 215                 220
276 Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val
277 225                 230                 235                 240
279 Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala
280                 245                 250                 255
282 Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val
283             260                 265                 270
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292 305                 310                 315                 320
294 Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met Gln
295                 325                 330                 335
297 Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys
298             340                 345                 350
300 Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe
301         355                 360                 365
303 Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu
304     370                 375                 380
306 Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe Phe
307 385                 390                 395                 400
309 Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu
310                 405                 410                 415
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313             420                 425                 430
315 Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly His
316         435                 440                 445
318 His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr
319     450                 455                 460
321 Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro
322 465                 470                 475                 480
324 Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val Pro
325                 485                 490                 495
327 His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser Arg
328             500                 505                 510
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331         515                 520                 525
333 Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu Ile
334     530                 535                 540
336 Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala
337 545                 550                 555                 560
339 Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu
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